Metabolic flux analysis cooperated with ^{13}C labeling experimentand constraint-based flux analysis

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Metabolic flux analysis has been widely used for quantification of cellular biochemical flux in metabolic engineering field[1]. This approach is very important for enhancing the understanding of biological system and generating experimental hypotheses. Thus a key issue that may arise in the application of flux analysis is more accurate calculation for the various given conditions. Regardless the existence of alternate optimal solution set that satisfy all of the constraints and have the same objective value, generally constraint-based flux analysis based on linear or quadratic programming is used for quantifying cellular fluxes[2,3]. However we have a few constraints from fermentation profiles and it can not guarantee the precisely calculated flux distribution. Herein, we carried out flux analysis with ^{13}C labeling experiment to determine *in vivo* flux distribution for central metabolic pathway and performed genome-scale constraints-based flux analysis with *in vivo* flux distribution as additional constraints which was reference flux values for quadraticprogramming. In addition, we demonstrated the extent of flux variability that could provide reliability of newly calculated flux distribution. Consequently, we had almost credible and global flux distribution of *E. coli* biochemical network through integrated approach which was combined constraint-based flux analysis with in vivo flux distribution from isotopomer analysis. This work was supported by the Korean Systems Biology Research Grant (M10309020000-03B5002-00000) from the MOST. Further supports by the BK21 program, LG Chemicals Chair Professorship and IBM SUR program are appreciated.

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